

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:17:05 ; Search time 17.21 Seconds
(without alignments)
112.588 Million cell updates/sec

Title: US-09-331-631A-22_COPY_25_84
Perfect score: 350
Sequence: 1 EDNNHHHGHGKSGQCVRRG.....EKKRGRSRHEADRDGSGSS 60

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	346	98.9	573	1	GLBL_MAIZE
2	81.5	23.3	605	1	VCLA_GOSHI
3	78	22.3	494	1	SFR4_GOSHI
4	71	20.3	699	1	SRCH_HUMAN
5	69.5	19.9	241	1	Y087_CAEEL
6	69	19.7	407	1	IE68_HVSA
7	69	19.7	588	1	VCLA_GOSHI
8	68.5	19.6	1407	1	TRHY_RABIT
9	67.5	19.3	466	1	CTP8_CAEEL
10	66	18.9	2339	1	CCAB_HUMAN
11	66	18.9	2339	1	CCAB_RABIT
12	65.5	18.7	345	1	VU79_HSV62
13	65.5	18.7	520	1	ITSN_HUMAN
14	65.5	18.7	2222	1	CCAE_RAT
15	65.5	18.7	2272	1	CCAE_MOUSE
16	65.5	18.7	2312	1	CCAE_MOUSE
17	65	18.6	107	1	HSP2_MOUSE
18	65	18.6	1130	1	REPT_MOUSE
19	63.5	18.1	520	1	LEG2_PEA
20	63.5	18.1	2505	1	CCAA_HUMAN
21	63	18.0	311	1	OSTP_RABIT
22	63	18.0	330	1	RLX3_STAU
23	63	18.0	344	1	SFR6_HUMAN
24	63	18.0	380	1	RDP_HUMAN
25	63	18.0	467	1	RXRG_CHICK
26	63	18.0	632	1	CCB2_RABIT
27	63	18.0	747	1	TRIS_ECOLI
28	62.5	17.9	103	1	HSP2_MACNE
29	62.5	17.9	517	1	LEGA_PEA
30	62.5	17.9	520	1	GAG_HV28
31	62	17.7	524	1	SBP_SOYEN
32	62	17.7	623	1	PNT1_DROME
33	62	17.7	654	1	CIK4_MUSPF

34	62	17.7	852	1	SRCH_RABIT	P16230 oryctolagus
35	62	17.7	1549	1	TRHY_SHEEP	P22793 ovis aries
36	61.5	17.6	522	1	GAG_HV261	P18041 human immun
37	61.5	17.6	550	1	BLSA_HUMAN	O02832 homo sapien
38	61.5	17.6	1234	1	CPAH_MOUSE	P06909 mus musculu
39	61	17.4	617	1	YACH_ECOLI	P36682 escherichia
40	61	17.4	1097	1	CCT_DROME	O96433 drosophila
41	61	17.4	1898	1	TRHY_HUMAN	O07283 homo sapien
42	61	17.4	2327	1	CCAB_MOUSE	O55017 mus musculu
43	60.5	17.3	33	1	MBPL_MAIZE	P28794 zea mays (m
44	60.5	17.3	195	1	AANT_HDVS1	P25883 hepatitis d
45	60.5	17.3	195	1	AANT_HDVS2	P25884 hepatitis d

ALIGNMENTS

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RESULT 1
GLBL_MAIZE STANDARD; PRT: 573 AA.
AC P15590;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE GLOBULIN-1 S ALLELE PRECURSOR (GLBI-S) (7S-LIKE).
GN GBL1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:CV. INBRED LINE VA26;
RA Belanger F.C., Kriz A.L.;
RT "Molecular characterization of the major maize embryo globulin encoded
RT by the Gbl1 gene."
RL Plant Physiol. 91:656-643(1989).
RM [2]
RN RP
RP MEDLINE:89374022; PubMed:2775172;
RA Kriz A.L.;
RT "Characterization of embryo globulins encoded by the maize Glb
RT genes."
RL Biochem. Genet. 27:239-251(1989).
CC -I- PWM: THREE PROTEIN-PROCESSING STEPS OCCUR IN THE FORMATION OF THE
CC MATURE PROTEIN FROM THE PRIMARY TRANSLATION PRODUCT.
CC -I- POLYMORPHISM: THE THREE MOST COMMONLY OCCURRING GLBI ALLELES HAVE
CC THE DESIGNATION L, I, AND S FOR LARGE, INTERMEDIATE, AND SMALL
CC PROTEINS, RESPECTIVELY.
CC -I- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
CC CONVICILIN, CONGLICININ, ETC.).
CC -----
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CC -----
DR EMBL; M24845; AAA33467.1; -.
DR HSSP; P50477; ICAM.
DR MAZEDB; 30181; -.
DR INTERPRO: IPR001113; -.
DR PRAM; PF00546; Seedstore_7s; 1.
KW Seed storage protein; Signal.
FT SIGNAL 1 18 OR 21 (POTENTIAL).
FT PROPEP 19 86
FT CHAIN 87 573 GLOBULIN-1 S ALLELE.
FT CARBOHYD 349 349 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 573 AA; 65029 MW; 525ED1DD0A062976 CRC64;
Query Match 98.9%; Score 346; DB 1; Length 573;

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RT protein, and localization of the gene to human chromosome 19 and
RL mouse chromosome 7.
CC Genomics 9:656-669(1991).
CC -1- FUNCTION: HEP MAY PLAY A ROLE IN THE REGULATION OF CA(2+)
CC SEQUESTRATION OR RELEASE IN THE SR OF SKELETAL AND CARDIAC
CC MUSCLE.
CC -1- SUBCELLULAR LOCATION: SARCOPLASMIC RETICULUM LUMEN.
CC -1- SIMILARITY: STRONG, TO RABBIT HRC.
CC -----
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CC -----
DR EMBL: M60052; AAA88071.1; -.
DR MIM: 142705; -.
KW Calcium-binding; Signal; Repeat; Polymorphism.
FT SIGNAL 1 28
FT CHAIN 29 699
FT FT SARCOPASMIC RETICULUM HISTIDINE-RICH
FT FT CALCIUM-BINDING PROTEIN.
FT FT GLU-RICH (ACIDIC).
FT FT ASP-RICH (ACIDIC).
FT FT 4 X TANDEM REPEATS, ACIDIC.
FT FT 1-1.
FT FT 1-2.
FT FT 1-3.
FT FT 1-4.
FT FT 6 X APPROXIMATE TANDEM REPEATS.
FT FT 2-1.
FT FT 2-2.
FT FT 2-3.
FT FT 2-4.
FT FT 2-5.
FT FT 2-6.
FT FT METAL-BINDING (POTENTIAL).
FT FT S -> V.
FT FT VARIANT 96
FT FT /FTID=VAR_005623.
SQ SEQUENCE 699 AA; 80244 MW; 9922EEDF012C61DD CRC64;

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Query Match 20.3%; Score 71; DB 1; Length 699;
Best Local Similarity 24.2%; Pred. No. 3.5;
Matches 22; Conservative 7; Mismatches 28; Indels 34; Gaps 3;

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OY 1 EDNNHNG-----GHS-----GCVRCRDRPM----- 26
DB 413 EVPHNNHVRPEDEVSATLGHQAPSHROSDDETGHGQSGSIKEMSHNPRGHTVVK 472
OY 27 QRPRLCEQREERKROERSHNEADDRSGE 57
DB 473 DRSHLRKDDSEERKEKEDPSHEEDDESSE 503

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RESULT 5
Y087_CAEEL STANDARD; PRT; 241 AA.
AC P34623;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HYPOTHEICAL 28.5 KDA PROTEIN ZK1236.7 IN CHROMOSOME III.
GN ZK1236.7
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabdilitida;
OC Rhabdilitida; Pelodermidae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

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RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner R., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Lattelle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Riken L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Mohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
CC -----
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CC -----
DR EMBL: L13200; AAA28188.1; -.
DR PIR: S44893; S44893.
DR WORMPEP: ZK1236.7; CE00384.
KW Hypothetical protein.
SQ SEQUENCE 241 AA; 28541 MW; 610ECA6537159FA7 CRC64;

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Query Match 19.9%; Score 69.5; DB 1; Length 241;
Best Local Similarity 41.9%; Pred. No. 1.9;
Matches 18; Conservative 9; Mismatches 9; Indels 7; Gaps 2;

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OY 17 VRCEDRPMHQRPCLEQREERERK--QERSHNEADDRSGE 57
DB 65 MREYEVREERERK---REERERKDEERAREADEAKAE 102

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RESULT 6
IE68_HSVSA STANDARD; PRT; 407 AA.
AC Q01042;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE IMMEDIATE-EARLY PROTEIN.
GN 73 OR ECLF1.
OS Herpesvirus saimiri (strain 11).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92333686; PubMed=1321287;
RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
RA Newman C., Wiltmann S., Craxton M.A., Coleman H., Fleckenstein B.,
RA Honess R.W.;
RT "Primary structure of the herpesvirus saimiri genome.";
RT J. Virol. 66:5047-5056(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92230228; PubMed=1314457;
RA Nicholas J., Cameron K.R., Coleman H., Newman C., Honess R.W.;
RT "Analysis of nucleotide sequence of the rightmost 43 kbp of
RT herpesvirus saimiri (HVS) L-DNA: general conservation of genetic
RT organization between HVS and Epstein-Barr virus.";
RL Virology 188:296-310(1992).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-1 AND
CC HSV-2 IE-68 (US1), EBV-1 65, EBV-4 (ORF4), PRV RSP40, AND VZV 63.
CC -----
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CC -----
DR EMBL: X64346; CAA45696.1; -
DR EMBL: M86409; AAA46149.1; -
DR EMBL: S75368; AAB21116.1; -
DR PIR: G36813; EDBEQ3.
DR PIR: S20244; S20244.
DR HSSP: P53041; 1A17.
KM Early protein.
FT DOMAIN 60
SQ SEQUENCE 407 AA; 46617 MW; FFD399CA82CE136C CRC64;

Query Match 19.7%; Score 69; DB 1; Length 407;
Best Local Similarity 45.7%; Pred. No. 3.4;
Matches 16; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 26 HORPCL--ECCREERERKQERSRHEADRSREG 58
   11: 1 11111 1:111 1:111
   52 HQQAALTEQRREVEGEGERERGRGEEREGC 86

RESULT 7
VCLB_GOSHI STANDARD; PRT; 588 AA.
AC P09801;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VICILIN C72 PRECURSOR (ALPHA-GLOBULIN B).
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Malvales; Malvaceae; Gossypium.
RN [1]
RP SEQUENCE FROM N.A.
RA Chlan C.A., Pyle J.B., Legocki A.B., Dure L. III;
RT "Developmental biochemistry of cottonseed embryogenesis and
RT germination. XVIII. cDNA and amino acid sequences of the members of
RT the storage protein families."
RL Plant Mol. Biol. 7:475-489(1986).
CC -1- FUNCTION: SEED STORAGE PROTEIN.
CC -1- SUBCELLULAR LOCATION: CYTOSOL; MEMBRANE-BOUND VACUOLAR PROTEIN
CC BODIES.
CC -1- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASOLIN, VICILIN,
CC CONVICILIN, CONGLICININ, ETC.).
CC -----
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CC -----
DR EMBL: M16891; AAA33071.1; -
DR PIR: A30838; FMCNAB.
DR HSSP: P50477; ICAX.
DR INTERPRO: IPR001113; -
DR PFAM: PF00546; Seedstore_7s; 1.
KW Seed storage protein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 588 VICILIN C72.
SQ SEQUENCE 588 AA; 69729 MW; 63E699B29AB8ADEB CRC64;

Query Match 19.7%; Score 69; DB 1; Length 588;
Best Local Similarity 30.6%; Pred. No. 4.7;
Matches 15; Conservative 12; Mismatches 16; Indels 6; Gaps 3;

QY 15 QCVARC---EDRPMDRPRCLCECCREERERK--RQERSRHEADRSREG 58

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DB 126 ECHOHQEQRP-ERKQCVRECRERYQENPMWRREBEAEFEETEG 173
   1: 1 111 1:111 1:111
   126 ECHOHQEQRP-ERKQCVRECRERYQENPMWRREBEAEFEETEG 173

RESULT 8
TRNH_RABIT STANDARD; PRT; 1407 AA.
ID TRNH_RABIT
AC P37709;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TRICHOHYALIN.
GN THH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RA Fietz M.J., Rogers G.E.;
RL Submitted (DEC-1992) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES
CC IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE
CC INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR
CC LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY
CC ISODIPEPTIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER
CC WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN
CC ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN
CC ITS OWN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINAL
CC DIFFERENTIATION.
CC -1- SUBUNIT: HOMODIMER (PROBABLE).
CC -1- TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES SUCH AS
CC THE INNER ROOT SHEAT (IRS) OF HAIR FOLLICLES AND MEDULLA, AND IN
CC THE FILIFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE).
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OF
CC THE EPIDERMIS.
CC -1- DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND
CC CALCIUM-BINDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST
CC ENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS
CC OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE STRANDED
CC ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS
CC THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS.
CC DOMAINS 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN
CC THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG
CC DIFFERENT SPECIES.
CC -1- PTM: KNOWN SUBSTRATE OF TRANSGUTAMINASE. SOME 200 ARGININES ARE
CC PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMINASE.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE S-100
CC FAMILY.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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CC -----
DR EMBL: Z19092; CAA79519.1; -
DR PIR: S28589; S28589.
DR HSSP: P02633; 1BQC.
DR INTERPRO: IPR001751; -
DR INTERPRO: IPR002048; -
DR PFAM: PF01023; S_100; 1.
DR PFAM: PF00036; efhand; 1.
DR PROSITE: PS00018; EF_HAND; 1.
DR PROSITE: PS00303; S100_CABP; 1.
KW Repeat; Calcium-binding.
FT DOMAIN 1 91
FT CA_BIND 22 33 SITE I (LOW AFFINITY) (POTENTIAL).
FT CA_BIND 62 73 SITE II (HIGH AFFINITY) (POTENTIAL).
SQ SEQUENCE 1407 AA; 183781 MW; AE17D2A159F12B7F CRC64;

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DR EMBL: M94172: AAA51897.1: -
 DR EMBL: M94173: AAA51898.1: -
 DR EMBL: U76666: AAC51138.1: -
 DR MIM: 601012: -
 DR INTERPRO: IPR000636: -
 DR INTERPRO: IPR002077: -
 DR PFM: PF00520: Ion trans: 4.
 DR PRINTS: PRO0167: CACCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; ATP-binding; Alternative splicing.
 FT REPEAT 82 359
 FT REPEAT 468 712
 FT REPEAT 1137 1419
 FT REPEAT 1456 1711
 FT DOMAIN 1 95
 FT TRANSMEM 96 114
 FT DOMAIN 115 132
 FT TRANSMEM 133 152
 FT DOMAIN 153 163
 FT TRANSMEM 164 183
 FT DOMAIN 184 187
 FT TRANSMEM 188 206
 FT DOMAIN 207 225
 FT TRANSMEM 226 245
 FT DOMAIN 246 331
 FT TRANSMEM 332 356
 FT DOMAIN 357 482
 FT TRANSMEM 483 501
 FT TRANSMEM 502 516
 FT TRANSMEM 517 536
 FT DOMAIN 537 544
 FT TRANSMEM 545 562
 FT DOMAIN 563 573
 FT TRANSMEM 574 592
 FT DOMAIN 593 611
 FT TRANSMEM 612 631
 FT DOMAIN 632 684
 FT TRANSMEM 685 709
 FT DOMAIN 710 1151
 FT TRANSMEM 1152 1169
 FT DOMAIN 1170 1185
 FT TRANSMEM 1186 1205
 FT DOMAIN 1206 1217
 FT TRANSMEM 1218 1236
 FT DOMAIN 1237 1246
 FT TRANSMEM 1247 1265
 FT DOMAIN 1266 1284
 FT TRANSMEM 1285 1304
 FT DOMAIN 1305 1391
 FT TRANSMEM 1392 1416
 FT DOMAIN 1417 1471
 FT TRANSMEM 1472 1490
 FT DOMAIN 1491 1505
 FT TRANSMEM 1506 1525
 FT DOMAIN 1526 1533
 FT TRANSMEM 1534 1552
 FT DOMAIN 1553 1563
 FT TRANSMEM 1564 1582
 FT DOMAIN 1583 1601
 FT TRANSMEM 1602 1621
 FT DOMAIN 1622 1683
 FT TRANSMEM 1684 1708
 FT DOMAIN 1709 2339
 FT TRANSMEM 2050 2054
 FT DOMAIN 2118 2122
 FT TRANSMEM 379 396
 NP BIND 451 458
 SITE 314 314

FT SITE 663 663 (BY SIMILARITY).
 FT SITE 1365 1365 (BY SIMILARITY).
 FT SITE 1655 1655 (BY SIMILARITY).
 FT SITE 1655 1655 (BY SIMILARITY).
 FT MOD_RES 1719 1719 (BY SIMILARITY).
 FT CA_BIND 1737 1748 (BY SIMILARITY).
 FT CARBOHYD 256 256 (BY SIMILARITY).
 FT CARBOHYD 1563 1563 (BY SIMILARITY).
 FT CARBOHYD 1675 1675 (BY SIMILARITY).
 FT VARSPLIC 2164 2339 (BY SIMILARITY).
 FT SEQUENCE 2339 AA: 262494 MW: 1744566DIE76B39D CRC64;

Query Match 18.9% Score 66; DB 1; Length 2339;
 Best Local Similarity 28.2%; Pred. No. 32;
 Matches 24; Conservative 7; Mismatches 14; Indels 40; Gaps 5;

OY 4 NHHHGGHKKSGCVRCEDEPRMRCLEO-----C 35
 DB 2050 HHHHH-----KCHRR-RDR-----KORSLEKPSLSADMDGAPSSAVGPGLPGEPTGC 2098
 OY 36 REEERERKORSRHEADDRSGEGSS 60
 DB 2099 R-REERERRGERSQERRRPSSSSS 2122

RESULT 11
 ID CCAB-RABIT STANDARD; PRT: 2339 AA.
 AC 005152;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BII).
 DE CACNA1B OR CACNA1A5 OR CACNS.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN:
 RX MEDLINE=93236885; PubMed=8386525;
 RA Fujita Y., Mylliclef M., Dirksen R.T., Kim M.-S., Nidome T., Nakai J., Friedrich T., Iabe N., Miyata T., Furutachi T., Furutake D., Mikoshiba K., Mori Y., Beam K.G.;
 RT "Primary structure and functional expression of the omega-conotoxin-sensitive N-type calcium channel from rabbit brain.";
 RL Neuron 10:585-598(1993).
 CC -I- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND BY OMEGA-AGATOXIN-DIHYDROXYDINES (DHP). THEY ARE HOWEVER INSENSITIVE TO CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN DIRECTED MIGRATION OF IMMATURE NEURONS.
 CC -I- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS

	CC	IN A 1:1-1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
	CC	-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
	CC	SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
	CC	CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/Delta
	CC	LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
	CC	I - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
	CC	I - TISSUE SPECIFICITY: WIDESPREAD EXPRESSION THROUGHOUT THE BRAIN,
	CC	HIGHEST LEVELS IN CORPUS STRIATUM AND MIDBRAIN.
	CC	I - DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
	CC	HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
	CC	POTIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
	CC	POSSIBLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
	CC	SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
	CC	I - PTM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND CGPK
	CC	(BY SIMILARITY).
	CC	I - SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
	CC	FAMILY.
	CC	-----
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	CC	the European Bioinformatics Institute. There are no restrictions on its
	CC	use by non-profit institutions as long as their content is in no way
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	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/)
	CC	or send an email to license@isb-sib.ch .
	CC	-----
	DR	EMBL; D14157; BAA03202.1; -.
	DR	INTERPRO; IPR000636; -.
	DR	INTERPRO; IPR002077; -.
	DR	PFAM; PF005520; Ion.trans. 4.
	DR	PRINTS; PR00167; CACCHANNE.
KW	MV	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW	KM	Calcium channel; Glycoprotein; Repeat; Multigene family;
FT	REPEAT	82 359
FT	REPEAT	469 713
FT	REPEAT	1142 1424
FT	REPEAT	1461 1714
FT	DOMAIN	1 95
FT	TRANSSEM	96 114
FT	DOMAIN	115 132
FT	TRANSSEM	133 152
FT	DOMAIN	153 163
FT	TRANSSEM	164 183
FT	DOMAIN	184 187
FT	TRANSSEM	188 206
FT	DOMAIN	207 225
FT	TRANSSEM	226 245
FT	DOMAIN	246 331
FT	TRANSSEM	332 356
FT	DOMAIN	357 483
FT	TRANSSEM	484 502
FT	DOMAIN	503 517
FT	TRANSSEM	518 537
FT	DOMAIN	538 545
FT	TRANSSEM	546 563
FT	DOMAIN	564 574
FT	TRANSSEM	575 593
FT	DOMAIN	594 612
FT	TRANSSEM	613 632
FT	DOMAIN	633 683
FT	TRANSSEM	686 710
FT	DOMAIN	711 1156
FT	TRANSSEM	1157 1174
FT	DOMAIN	1175 1190
FT	TRANSSEM	1191 1210
FT	DOMAIN	1211 1222
FT	TRANSSEM	1223 1241
FT	DOMAIN	1242 1251
FT	TRANSSEM	1252 1270
FT	DOMAIN	1271 1289
FT	TRANSSEM	1290 1309
FT	DOMAIN	1310 1396

FT	TRANSMEM	1397	1421	S6 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1422	1476	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1477	1495	S1 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1496	1510	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1511	1530	S2 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1531	1538	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1539	1557	S3 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1558	1566	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1567	1585	S4 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1586	1604	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1605	1624	S5 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1625	1686	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1687	1711	S6 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1712	2339	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	2051	2055	POLY-HIS.
FT	DOMAIN	2119	2123	POLY-SER.
FT	DOMAIN	2319	2324	POLY-GLY.
FT	DOMAIN	379	396	BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT	NP_BIND	452	459	APP (POTENTIAL).
FT	SITE	314	314	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	663	663	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1370	1370	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1658	1658	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	MOD_RES	1722	1722	PHOSPHORYLATION (BY GAPK) (POTENTIAL).
FT	CA_BIND	1740	1751	BY SIMILARITY.
FT	CARBOHYD	256	256	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1566	1566	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1678	1678	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	2339	AA: 261178	MM: 040130A53794C8B54 CRC54;

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Query Match          18.9%; Score 66; DB 1; Length 2339;
Best Local Similarity 28.2%; Pred. No. 32;
Matches    24; Conservative   7; Mismatches    14; Indels    40; Gaps    5;

QY      4 NHHHGHKSGCVCRCEDRPWHQRPCLEQ-----C 35
       :| | | : | | | : | | : | | : |
Db- 2051 HHHHH-----RCHRR-RDR----KQSLKEGPKSLADTDGAPDSTVGRLPTGGPPCC 2099
                                     |
QY      36 REERERKQERSRHADRDGSGEGSS 60
       ||||| | | | : : | |
Db- 2100 R-RERERROERGSRQERRROPSSSSS 2123

RESULT 12
VU79_HSV6Z STANDARD; PRT; 345 AA.
AC P52530;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROTEIN U79.
GN GN CB7R.
OS Herpes simplex virus (type 6 / strain Z29).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
RN (1)
RA MEDLINE=96195263; PubMed=8634027;
RA Lindquester G.J., Inoue N., Allen R.D., Castelli J.W.,
RA Stramey F.R., Dambaugh T.R., O'Brian J.J., Danovich R.M.,
RA Frankel N., Pellett P.E.;
RT "Restriction endonuclease mapping and molecular cloning of the human
RT herpesvirus 6 variant B strain Z29 genome." ;
RL Arch. Virol. 141:367-379(1996).
CC -!- FUNCTION: POSSIBLE REPLICATION PROTEIN.
CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-6 AND
CC HSV-7 U79 AND HCMV UL12 (P3)

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DR EMBL: L14772; AAB06363.1; -
 CC
 DR SEQUENCE 345 AA: 39579 MW: E2CC942C85D4975C CRC64:

Query Match 18.7%; Score 65.5; DB 1; Length 345;
 Best Local Similarity 26.4%; Pred. No. 6.5;
 Matches 14; Conservative 14; Mismatches 14; Indels 11; Gaps 2;

QY 2 DDHHNHGKSGOCVRCEDRWQRRPCLDCCREERERKROERSHEDDR 54
 DB 161 DDEHRRKSGKQKER--RKVED-----IDKKKEDEKRRKQKRRNDEDKR 202

RESULT 13

ITSN_HUMAN STANDARD; PRT; 520 AA.

AC 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERSECTIN (SH3 DOMAIN-CONTAINING PROTEIN SH3P17).
 GN ITSN OR SH3D1A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 [1]

RP SEQUENCE FROM N.A.
 RC TISSUE-BONE MARROW;
 RX MEDLINE=98294438; PubMed=9630982;
 RA Sparks A.B., Hoffman N.G., McConnell S.J., Fowlkes D.M., Kay B.K.;
 RT "Cloning of ligand targets: systematic isolation of SH3 domain-
 RT containing proteins.";
 RL Nat. Biotechnol. 14:741-744(1996).
 RN [2]

RP GENE MAPPING.
 RX MEDLINE=98127038; PubMed=9465890;
 RA Chen H., Antonarakis S.E.;
 RT "The SH3D1A gene maps to human chromosome 21q22.1-->q22.2.";
 CC Cytogenet. Cell Genet. 78:213-215(1997).
 CC -1- SIMILARITY: CONTAINS 4 SH3 DOMAINS.

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DR EMBL: U61166; AAC50592.1; -
 DR HSSP: P29354; IGFED.
 DR MIM: 602442; -
 DR INTERPRO: IPR001452; -
 DR PFAM: PF00018; SH3; 4.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PROSITE: PS00002; SH3; 4.
 KW SH3 domain; Repeat.
 FT DOMAIN 116 177 SH3.
 FT 284 342 SH3.
 FT DOMAIN 374 438 SH3.
 FT 455 514 SH3.
 FT DOMAIN 520 AA: 57976 MW: 614043F1DB098C60 CRC64:
 CC SEQUENCE

Query Match 18.7%; Score 65.5; DB 1; Length 520;
 Best Local Similarity 33.9%; Pred. No. 9.4;
 Matches 19; Conservative 9; Mismatches 11; Indels 17; Gaps 4;

QY 18 RCE--DRP-----HQRPRCL--EQCREERERK--OERSRHEDDRSG 56
 DB 27 RRAQERDKWLEHVOEDEHORPRKLHEERLKRRESYVKKDEGKQKQKQKLG 82

RESULT 14

CCAE RAT STANDARD; PRT; 2222 AA.

AC 007652;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE VOLTAGE-DEPENDENT R-TYPE CALCIUM CHANNEL ALPHA-1E SUBUNIT (CALCIUM
 DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE, ISOFORM 6) (RBE-11) (RBE2)
 GN (BRAIN CALCIUM CHANNEL 11) (B11).
 GN CACNA1E OR CACNL1A6 OR CACHE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
 RX MEDLINE=93262464; PubMed=838125;
 RA Soong T.W., Stea A., Hodson C.D., Dubel S.J., Vincent S.R.,
 RA Snutch T.P.;
 RT "Structure and functional expression of a member of the low voltage-
 RT activated calcium channel family.";
 RL Science 260:1133-1136(1993).

CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E
 CC BELONGS TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
 CC BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA).
 CC THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), OMEGA-
 CC CONOTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-
 CC AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE
 CC INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS
 CC IMPORTANT FOR INFORMATION PROCESSING.

CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
 CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE POR-
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN CENTRAL NERVOUS SYSTEM AND IN
 CC INSULINOMA.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 CC FAMILY.

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DR EMBL: L15453; AAA0855.1; -
 DR INTERPRO: IPR000636; -

DR INTERPRO: IPR002077; .
 DR PIRAM; Pf00520; Ion_trans; 4.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation.
 FT REPEAT 27 305 I.
 FT REPEAT 413 657 II.
 FT REPEAT 1092 1378 III.
 FT REPEAT 1415 1678 IV.
 FT DOMAIN 1 40
 FT TRANSSEM 41 59
 FT DOMAIN 60 78
 FT TRANSSEM 79 97
 FT DOMAIN 98 109
 FT TRANSSEM 110 124
 FT DOMAIN 125 136
 FT TRANSSEM 137 156
 FT DOMAIN 157 174
 FT TRANSSEM 175 195
 FT DOMAIN 196 277
 FT TRANSSEM 278 301
 FT DOMAIN 302 427
 FT TRANSSEM 428 447
 FT DOMAIN 448 460
 FT TRANSSEM 461 480
 FT DOMAIN 481 489
 FT TRANSSEM 490 508
 FT DOMAIN 509 518
 FT TRANSSEM 518 537
 FT DOMAIN 538 556
 FT TRANSSEM 557 576
 FT DOMAIN 577 629
 FT TRANSSEM 630 654
 FT DOMAIN 655 1100
 FT TRANSSEM 1101 1117
 FT DOMAIN 1118 1141
 FT TRANSSEM 1142 1161
 FT DOMAIN 1162 1192
 FT TRANSSEM 1193 1206
 FT DOMAIN 1207 1224
 FT TRANSSEM 1225 1243
 FT DOMAIN 1244 1263
 FT TRANSSEM 1264 1350
 FT DOMAIN 1351 1374
 FT TRANSSEM 1375 1431
 FT DOMAIN 1432 1450
 FT TRANSSEM 1451 1467
 FT DOMAIN 1468 1485
 FT TRANSSEM 1486 1493
 FT DOMAIN 1494 1512
 FT TRANSSEM 1513 1523
 FT DOMAIN 1524 1542
 FT TRANSSEM 1543 1561
 FT DOMAIN 1562 1581
 FT TRANSSEM 1582 1650
 FT DOMAIN 1651 1676
 FT TRANSSEM 1677 2222
 FT DOMAIN 667 672
 FT TRANSSEM 699 704
 FT DOMAIN 718 723
 FT TRANSSEM 1058 1064
 FT DOMAIN 1180 1183
 FT TRANSSEM 2193 2196
 FT DOMAIN 325 342
 FT SITE 260 260
 FT SITE 608 608
 FT SITE 1324 1324

FT SITE 1615 1615 CALCIUM ION SELECTIVITY AND PERMEABILITY
 FT CA_BIND 377 389 (BY SIMILARITY).
 FT MOD_RES 1686 1686 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT CA_BIND 1704 1715 BY SIMILARITY.
 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1518 1518 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1523 1523 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1641 1641 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 2222 AA: 252114 MM; DP6452A2175CEB19 CMC64;
 Query Match 18.7%; Score 65.5; DB 1; Length 2222;
 Best Local Similarity 32.4%; Pred. No. 34;
 Matches 23; Conservative 9; Mismatches 24; Indels 15; Gaps 4;
 QY 3 DNHMHGHSQCVR-RCEDRPWHRPCLEOCREER-----EKROERS---R 48
 Db 1977 DSGHKSPTHRSGRGERSKERK-HLSPVSRNCSERGTQADWESPERSRSPSEGR 2035
 OY 49 HEADRSGEGS 59
 Db 2036 SQTPNRGTGS 2046
 RESULT 15
 CCAL_MOUSE STANDARD; PRT: 2272 AA.
 ID CCAL_MOUSE
 AC 061250;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE VOLTAGE-DEPENDENT R-TYPE CALCIUM CHANNEL ALPHA-1E SUBUNIT (CALCIUM
 CHANNEL, L-TYPE, ALPHA-1 POLYPEPTIDE, ISOFORM 6) (BRAIN CALCIUM
 DE CHANNEL II) (B11).
 GN CACNAIE OR CCHRA1 OR CACNM1A6 OR CACHE6.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE=94350992; Pubmed=8071363;
 RA Williams M.E., Marubio L.M., Deal C.R., Hans M., Brust P.F.,
 RA Philipson L.H., Muller R.J., Johnson E.C., Harpold M.M., Ellis S.B.;
 RT "Structure and functional characterization of neuronal alpha 1E
 RT calcium channel subtypes.";
 RL J. Biol. Chem. 269:22347-22357(1994).
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E
 CC GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS
 CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
 CC BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-ITIA (OMEGA-AGA-ITIA).
 CC THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), OMEGA-
 CC CONTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-
 CC AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE
 CC INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS
 CC IMPORTANT FOR INFORMATION PROCESSING.
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
 CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNTS
 CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE FOR-
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNTS BETA AND ALPHA-2/DELTA
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURONAL TISSUES, RETINA, SPLEEN,
 CC AND PANCREATIC ISLET CELLS.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE

